In the Claims

Applicant has submitted a new complete claim set showing marked up claims with insertions indicated by underlining and deletions indicated by strikeouts and/or double bracketing.

Please amend pending claims 1, 2, 7-10, 20, and 25 as noted below.

1. (Currently Amended) A method for identifying at least one human coding region/gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder, comprising:

identifying the position ~~positions~~ of a coding region/gene ~~regions/genes~~ in an 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof that can be compared to an ~~the~~ equivalent region ~~regions~~ of DNA from a person afflicted with a mood disorder or a related disorder, and~~.~~

detecting differences between the coding region/gene ~~regions/genes~~ of the 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof and equivalent region ~~regions~~ in the DNA of an individual afflicted with a mood disorder or related disorder, wherein a difference in the coding region/gene and the equivalent region ~~regions/genes is an indication that~~ identifies the coding region/gene or mutated or polymorphic variant thereof ~~is~~ as associated with the mood disorder or related disorder.

2. (Currently Amended) A method for identifying at least one human coding region/gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder, comprising:

identifying the position ~~positions~~ of a coding region/gene ~~regions/genes~~ in a YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers D18S60 and D18S61 that can be compared to an ~~the~~ equivalent region ~~regions~~ of DNA from a person afflicted with a mood disorder or a related disorder, and~~.~~

detecting differences between the coding region/gene ~~regions/genes~~ of the YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers

D18S60 and D18S61 and the equivalent region of ~~regions in the~~ DNA of an individual afflicted with a mood disorder or related disorder, wherein a difference in the coding region/gene and the equivalent region of DNA ~~regions/genes is an indication~~ identifies that the coding region/gene or mutated or polymorphic variant thereof is associated with the mood disorder or related disorder.

3. (Previously Presented) The method of claim 2 wherein said portion comprises the region of chromosome 18q between polymorphic markers D18S68 and D18S979 or a fragment of said region.

4. (Currently Amended) The method of claim 2 wherein said YAC clone is 961_h_9, 942_c_3, 766_f_12, 731_c_7, 907_e_1, ~~752-g-8~~ 752_g_8 or 717_d_3.

5. (Previously Presented) The method of claim 4 wherein said YAC clone is 961_h_9, 766_f_12 or 907_e_1.

6. (Previously Presented) The method of claim 1 wherein said mood disorder or related disorder is selected from the group consisting of: mood disorders, schizophrenia and related disorders, anxiety disorders, adjustment disorders and personality disorders.

7. (Currently Amended) A method of identifying at least one human coding region/gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder which comprises:

detecting a nucleotide triplet repeat ~~repeats~~ in a region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979, wherein the presence of the nucleotide triplet repeat ~~repeats~~ in a region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 identifies ~~indicates~~ the presence of a human coding region/gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder.

8. (Currently Amended) A method of identifying at least one human coding region/gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder comprising:

transforming a YAC clone with a linearized YAC fragmentation vector containing a portion of human chromosome 18q disposed between the markers D18S60 and D18S61 ~~triplet repeats~~,

identifying a transformed YAC clone containing a portion of human chromosome 18q disposed between the markers D18S60 and D18S61 ~~triplet repeats~~,

determining ~~a sequence flanking the triplet repeats~~ the presence of trinucleotide repeats in the sequence between the markers D18S60 and D18S61, and

comparing the sequence to an equivalent region of DNA from a person afflicted with a mood disorder or a related disorder, wherein a difference in the ~~sequence flanking the triplet repeats and the DNA~~ presence of trinucleotide repeats in the YAC clone DNA sequence between markers D18S60 and D18S61 and the equivalent region of DNA from the afflicted person identifies ~~is an indication of~~ the presence of a human coding region/gene or mutated or polymorphic variant thereof that is associated with the mood disorder or related disorder.

9. (Currently Amended) A method as claimed in claim 7 wherein the ~~said~~ triplet repeat is CAG or CTG.

10. (Currently Amended) A method as claimed in claim 9 wherein the ~~said~~ triplet repeat is detected by means of a probe comprising at least 5 CTG and/or CAG repeats.

11-19. (Cancelled)

20. (Currently Amended) A method for detection in a patient of a pathological mutation or genetic variation associated with a mood disorder or related disorder, comprising:

hybridizing a probe of at least 14 contiguous nucleotides of a cDNA encoded by a coding region/gene identified ~~obtained~~ by the method of claim 7 with a DNA sample from said patient and a DNA sample from a control individual who is not affected by a mood disorder or related disorder and does not have a family history of mood disorders, wherein the cDNA encodes a

human protein which if defective is associated with a mood disorder or related disorder and is the expression product of a human gene, including mutated or polymorphic variants thereof, that is associated with a mood disorder or related disorder, and

comparing the hybridization of the probe to the said patient sample with the hybridization of the probe in the control sample, wherein a difference in the hybridization of the probe in the patient indicates a pathological mutation or genetic variation associated with a mood disorder or related disorder.

21-24. (Cancelled)

25. (Currently Amended) A method of determining the susceptibility of an individual to a mood disorder or related disorder which method comprises:

a) obtaining a DNA sample from said individual;

b) providing primers suitable for the amplification of a nucleotide sequence comprised in the sequences shown in Figure 15a, (SEQ ID NO:12) said primers flanking the trinucleotide repeats comprised in said sequences;

c) applying said primers to the DNA sample and carrying out an amplification reaction;

d) applying said primers to a DNA sample from a control individual who is not affected by a mood disorder or related disorder and does not have a family history of mood disorders, and carrying out the amplification reaction; ~~and~~

e) determining the presence of a DNA polymorphism in the amplified products from the DNA sample and the sample from the control individual,

f) comparing the results of the amplification reaction for the individual and for the control individual;

wherein the presence of an amplified product that includes a DNA polymorphism associated with a mood disorder or related disorder in a region of chromosome 18q disposed between polymorphic markers D18S68 and D18S979 that is different in the individual sample than in the sample from the control individual is an indication of the presence of a susceptibility to a mood disorder or related disorder of said individual.

26. (Previously Presented) A method as in claim 25 wherein said DNA polymorphism is a trinucleotide repeat expansion.

27. (Previously Presented) A method as in claim 26 wherein said trinucleotide repeat expansion is comprised in a sequence of nucleotides that differ from the sequence of nucleotides shown in figure15a, (SEQ ID NO:12) only in said trinucleotide repeat expansion.

28. (Cancelled)

29. (Previously Presented) A method as in claim 25 wherein said nucleotide sequence to be amplified is comprised in the sequence shown in Figure 15a (SEQ ID NO:12) and said primers have the sequences shown in Figure 15b (SEQ ID NOs:13 and 14).

30-47. (Cancelled)